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Automated detection of internal parasitic eggs in cattle faecal sample using you only look once

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ABSTRACT

Parasitic infections pose a serious threat to livestock productivity, but controls have been hindered in regions with limited diagnostic infrastructure. This study aims to develop and evaluate an artificial intelligence (AI)-powered diagnostic tool based on you only look once version 11 (YOLOv11) integrated in Roboflow platform to facilitate the easy detection of four types of parasitic eggs including *Fasciola* sp., *Strongyle* sp., *Paramphistomum* sp., and *Moniezia* sp., in cow faecal samples. A total of 191 selected microscopic images were collected from various regions in Indonesia using smartphone-mounted microscopy, and subsequently labelled, manually annotated and augmented to 528 annotations using Roboflow. After training, the YOLOv11 model achieved mAP@50 of 98.0%, precision of 94.7%, and recall of 95.8% across 5-fold cross-validation. Class-wise results showed high recall values greater than 95%, with *Fasciola* sp. achieving 97% precision, *Moniezia* sp. 99%, and *Paramphistomum* sp. 100%, while *Strongyle* sp. showed moderate performance (82% and 66.7%). Comparative evaluation with YOLOv5 and YOLOv8 demonstrated similar but slightly improved performance using YOLOv11. These findings highlight the potential implementation of YOLOv11-based diagnostics for detecting internal parasitic eggs in cattle, particularly in resource-limited settings.

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1. INTRODUCTION

Parasitic infections remain a critical constraint to cattle industry and global food security. These infections reduce weight gain, milk production, carcass quality, cause infertility, liver condemnation, and increased treatment cost during increased morbidity in cattle [1]–[4]. Developing countries experience latent yet substantial burdens due to high infection rates [5]. However, the burdens and their impacts on production have been unnoticed [6], due to limited diagnostic capabilities in remote regions.

Traditional diagnostic methods rely on microscopic identification of parasite eggs in faecal samples. The methods are time-intensive in nature and need trained personnel. Time-intensive work can result in inconsistent results, high rates of diagnostic errors [7], [8], and false negative results [9], especially when a large number of sample size has to be examined. Moreover, the expertise is often unavailable in rural areas [10]. These diagnostic limitations highlight an urgent need for rapid, reliable, and accessible diagnostic methods that could replace the shortage of expertise in rural areas, to manage internal parasitosis more effectively and sustainably [11], [12].

Artificial intelligence (AI) through object detection algorithms based on convolutional neural networks (CNNs), has recently emerged as a robust technological alternative to traditional microscopic diagnostics. These AI techniques demonstrate remarkable capabilities in image recognition and classification tasks. Thus making them potentially useful for microscopic diagnostics involving parasite eggs [13]–[15]. The automated AI-driven diagnostics offers significant improvements in accuracy, reproducibility, and diagnostic throughput, and reducing the dependency on skilled human observers.

The deployment of an AI-based diagnostic system could fundamentally transform parasite management strategies in livestock production systems. Faster and more accurate diagnostics enable earlier intervention, reducing the prevalence and intensity of infections, and thereby improving animal welfare and productivity. This aligns with global efforts to enhance food security through improved animal health monitoring and disease control. Such systems could play a role in resistance management. The ability to monitor parasite loads more frequently may help detect emerging anthelmintic resistance, such as triclabendazole resistance in *Fasciola hepatica*, and enabling timely adjustments to treatment protocols.

In veterinary parasitology, CNN algorithms have been applied to detect fecal parasites in dogs and cats in clinical settings. These models successfully distinguished parasite eggs from fecal debris with 88% accuracy, identifying eggs of *Toxocara*, *Taenia*, and *Ancylostoma*. This demonstrates the potential of deep learning models for diagnostic applications and their ability to enhance diagnostic accuracy in veterinary medicine [8], [16]. In human medical diagnostics, CNN models such as YOLOv3, YOLOv4, YOLOv5, and InceptionResNetV2 are capable of rapidly and accurately identifying helminth eggs in human fecal samples and distinguishing them from fecal components that appear similar [7], [17], [18]. These findings indicate an opportunity to develop AI-based diagnostic tools for detecting internal parasites in other species.

A more recent YOLO architecture, YOLOv11, has garnered increasing attention for its enhanced detection speed, accuracy, and computational efficiency in real-time object detection applications across domains such as vehicle recognition and medical imaging. Thus, underscoring its adaptability and power in diagnostic tasks. Recent advancements suggest that YOLOv11 significantly outperforms earlier versions in complex visual environments, making it well-suited for image-based diagnostics. Further, YOLOv11 can be used in combination with Roboflow at https://roboflow.com, a cloud-based computer vision platform that enables model training, augmentation, and deployment [19]. YOLOv11 performs the detection task, and Roboflow facilitates dataset management and preprocessing, as well as hyperparameter optimization. The integration of YOLOv11 with transfer learning techniques amplifies its performance and enabling high-accuracy outcomes even with limited training data [20].

While there has been extensive research on CNNs for diagnostic development, studies regarding AI development for detecting internal parasites in cattle remain very limited. Therefore, this study aims to evaluate the diagnostic accuracy, precision, and robustness of YOLO and Roboflow in detecting four types of cattle parasite eggs, i.e *Fasciola* sp., *Strongyle* sp., *Paramphistomum* sp., and *Moniezia* sp. The evaluation utilizes the YOLO algorithm based on microscopic images captured via smartphone. This research is expected to contribute to the development of valid, mobile-compatible AI solutions to support the diagnosis of internal parasitic infections in cattle. The resulting evaluation aims to provide a faster, more consistent approach suitable for large-scale implementation in rural areas.

2. METHOD

2.1. Study design and workflow

This research employed an experimental diagnostic validation framework to develop and evaluate an automated system for detecting parasitic eggs in cattle faecal samples using YOLO. YOLO is one of a CNN-based object detection model. The proposed pipeline integrated the YOLO architecture with the Roboflow platform to optimize training, data preprocessing, and deployment. The process consist of several sequential stages: i) acquisition of microscopic images via smartphone-based microscopy; ii) annotation of parasite eggs; iii) dataset augmentation to enhance generalization; iv) model training using YOLO within Roboflow's cloud environment; and v) model evaluation based on standard performance metrics. Evaluation stage consisted of two steps: validation and testing.

In addition to a standard train, validation and test split, a 5-fold cross-validation strategy was implemented to evaluate model stability and generalization. Each fold preserved class balance across the four parasite categories, and performance metrics were averaged across the 5-folds. Since Roboflow does not support cross-validation natively, the cross-validation process was conducted locally on a computer equipped with an Intel Core i7 processor and an NVIDIA RTX 3050 GPU with 4 GB of memory. This structured

approach ensured methodological consistency and facilitated rigorous performance assessment. A schematic block diagram illustrating the workflow of the research is presented in Figure 1.

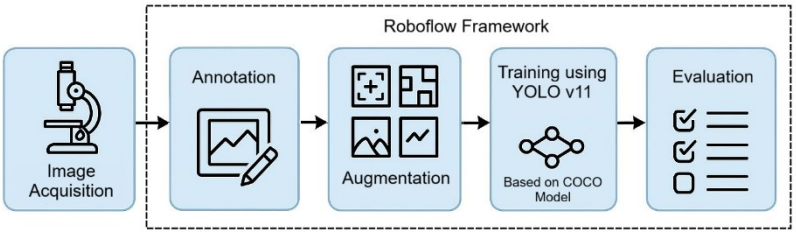


Figure 1. Block diagram of diagnostic development and validation framework using the combination of YOLOv11 and Roboflow

2.2. Sample collection and image acquisition

Four cattle parasitic classes were subjects of the study, namely *Fasciola* sp., *Paramphistomum* sp., *Moniezia* sp., and *Strongyle* sp. Samples of adult *Fasciola* sp., *Paramphistomum* sp., and *Moniezia* sp. were collected during post-mortem inspections of cattle slaughtered from several regions in Indonesia, such as Java, Sumatera, Kalimantan, and Sulawesi regions, Indonesia. Samples of adult *Fasciola* sp. were identified during a post-mortem inspection of livers in the abattoir. Samples of adult *Paramphistomum* sp. and *Moniezia* sp. were detected during postmortem inspection of cattle rumen and intestine in the abattoir. The faecal samples were also collected from the abattoir. The fresh adult helminths and faecal samples were kept at 4 °C, and immediately sent to the Laboratory of Veterinary Parasitology, Faculty of Veterinary Medicine, Universitas Brawijaya for processing.

The adult helminths were crushed, added with the same volume of the known parasitic-egg-free cattle faeces and with three-fold volume of aquadest, and processed with the sedimentation method. Briefly, the samples were strained using a 200 µm strainer followed by a 40 µm strainer. The sediment collected was immediately placed on an object glass and observed under a light microscope (CX23LEDRFS1, Olympus, Tokyo, Japan) at 40x objective magnification to confirm the presence of parasitic eggs. On the other hand, *Strongyle* sp. eggs were extracted from the faecal samples using the floatation method with 60% sucrose. The floated *Strongyle* sp. eggs were observed under the microscope for confirmation. Images of parasitic eggs were subsequently taken using a smartphone (Redmi 9™, Xiaomi, Haidian, Beijing, China) mounted to the ocular lens of the microscope. This method followed a low-cost diagnostic approach consistent with mobile-based diagnostics recommended for resource-limited environments [21]–[23]. The image files were kept in a digital file folder for further analysis.

2.3. Image annotation and augmentation

The images were annotated using the online Roboflow self-labelling platform. Each parasitic egg was delineated with a bounding box, following an established standard of object detection dataset preparation. Manual annotation ensured the inclusion of subtle morphological features for species differentiation. The process was conducted by an expert in veterinary parasitology. Bounding boxes served as the ground truth for supervised training, enabling the model to learn localization alongside classification. All microscopic images were manually annotated and validated through a consensus process by a panel of experts in veterinary parasitology to guarantee high ground-truth accuracy and diagnostic consistency across classes.

To enhance model robustness and generalization to application, the annotated dataset underwent augmentation using Roboflow's preprocessing tools. Augmentation techniques included: i) geometric transformations, horizontal and vertical flips, and rotations of 90°, to simulate diverse egg orientations; ii) scale and perspective changes, zoom up to 20% to replicate variation in egg size and microscope focusing; iii) photometric adjustments, exposure shifts (±10%) and saturation shifts (±25%) to accommodate differences in lighting conditions and staining; and iv) image blurring, Gaussian blur up to 2.5 pixels to mimic focus inconsistencies. Augmented data were then used for model training and validation. The techniques are known to mitigate overfitting and improve deep learning based diagnostic performance. A comparative experiment was performed to assess the impact of data augmentation. Two training configurations were evaluated: i) the original annotated dataset without augmentation and ii) the augmented dataset as previously described, to confirm the contribution of augmentation to performance improvement in small datasets.

2.4. Dataset splitting for model training and evaluation

For this study, the final dataset for each of the four parasite classes was divided into three groups. These groups were training, validation, and testing. This partitioning ensures proportional representation across the four classes. maintaining class balance during performance evaluation and preventing model bias toward classes with larger sample sizes [24].

2.5. Model architecture and comparative analysis

The YOLOv11 algorithm was selected for object detection, as it represents an evolution of previous YOLO versions. YOLOv11 incorporates deeper convolutional layers, an optimized anchor box mechanism, and refined feature extraction modules, making it well-suited for high-precision recognition tasks, such as the detection of internal parasite eggs. The Roboflow platform was utilized to assist in data preprocessing for training, offering integrated tools for dataset preprocessing, augmentation, model configuration, and deployment. Transfer learning was applied by leveraging a model pre-trained on the COCO dataset. This approach utilizes knowledge gained from large-scale object detection tasks to enhance the performance of a new system operating in a more specific domain with limited data. To validate the choice of YOLOv11, experiments were conducted comparing it against YOLOv5 and YOLOv8 using identical training configurations. Since these earlier YOLO versions are not supported by Roboflow, the experiments were performed locally to ensure implementation consistency and a fair comparison.

2.6. Training configuration and hyperparameters

The YOLOv11 model was trained on Roboflow's cloud infrastructure using the following optimized hyperparameters: i) input image size of 640 × 640 pixels; ii) number of epochs up to 250; and iii) confidence threshold of 0.5. These parameters were determined following an iterative optimization process, balancing training time with model convergence and accuracy. Training and validation losses were monitored throughout the process to ensure smooth convergence without overfitting, indicated by stable mean average precision (mAP@50) values.

2.7. Evaluation metrics and class-wise performance analysis

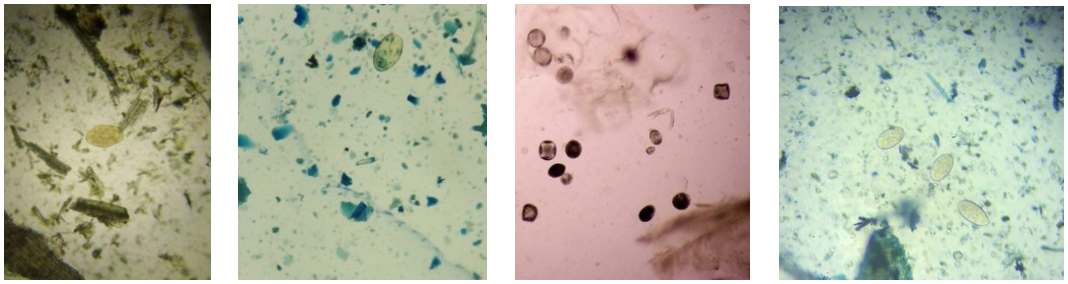
Model performance was evaluated using a held-out test set, based on standard object detection metrics, consist of: i) precision (or positive predictive value), representing the proportion of actual positive cases among all positive detections; ii) recall (or sensitivity), representing the proportion of correctly identified positive detections among all actual positive cases; iii) mAP@50, representing the average precision (AP) across all classes at an intersection over union (IoU) threshold of 0.5; and iv) confidence scores, representing probability estimates for each bounding box that reflect the model's level of certainty. Per-class performance was analyzed using a confusion matrix, enabling detailed error analysis and the identification of misclassification patterns, particularly among species with morphological similarities. Precision-recall (PR) curves were also generated to visualize the trade-off between recall (or sensitivity) across various confidence thresholds.

3. RESULTS AND DISCUSSION

3.1. Dataset composition and distribution

In total, 191 carefully selected microscopic images were produced. The resulting images exhibited resolutions ranging from 1080 × 1440 pixels to 3024 × 4032 pixels, ensuring adequate detail for subsequent object detection tasks. Representative microscopic images of cattle parasitic eggs evaluated in this study are shown in Figure 2, including *Strongyle* sp. in Figure 2(a), *Fasciola* sp. in Figure 2(b), *Moniezia* sp. in Figure 2(c), and *Paramphistomum* sp. in Figure 2(d). Using manual labelling, 528 annotated images were generated from 191 images. The distribution of raw and annotated images across parasite classes is presented in Table 1, comprising four target classes: *Fasciola* sp. (n = 89 annotated images), *Strongyle* sp. (n = 78), *Moniezia* sp. (n = 324), and *Paramphistomum* sp. (n = 37). Class imbalance was evident, particularly for *Paramphistomum* sp. and *Strongyle* sp.

To overcome imbalance class, augmentations were made, further expanding the dataset to 459 images. The final dataset of the 459 images was split into three subsets: i) training dataset 88% (n = 402 images); ii) validation dataset 6% (n = 29); and iii) testing dataset 6% (n = 28). The dataset was partitioned using stratified sampling to maintain consistent class proportions across the training, validation, and test sets, thereby preventing bias toward dominant classes. During the test, the automated system processed each image in under 0.5 seconds.



(a) (b) (c) (d)

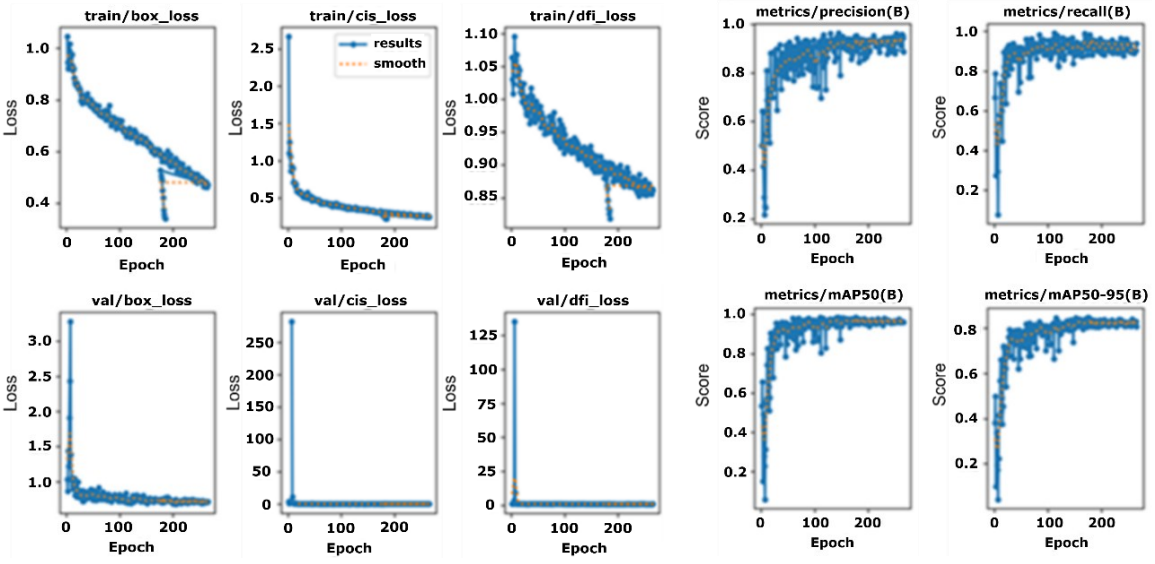
Figure 2. Microscopic images of cattle parasitic eggs for: (a) *Strongyle* sp., (b) *Fasciola* sp., (c) *Moniezia* sp., and (d) *Paramphistomum* sp.

Table 1. Sample distribution of the study of the development of an AI-powered detection of internal parasites of cattle using YOLOv11

Parasite type	No. of images	No. of annotated images	No. of augmented images
Fasciola sp.	86	89	202
Strongyle sp.	71	78	175
Moniezia sp.	9	324	21
Paramphistomum sp.	25	37	61
Total	191	528	459

3.2. Training and evaluation performances

The YOLOv11 model was trained on the augmented dataset comprising 459 images. Figure 3 displays overall training and evaluation performance of the YOLOv11 metrics over 250 epochs. Figure 3(a) shows training and validation loss curves (box loss, classification loss, and distribution focal loss) plotted against training epochs, and Figure 3(b) shows performance metrics including precision, recall, mAP@50, and mAP@50–95 plotted against epochs. Performance monitoring over 250 epochs demonstrated smooth convergence of both training and validation loss curves, indicating stable learning without signs of overfitting. The mAP at an IoU threshold of 0.5 (mAP@50) consistently improved throughout the early training stages, stabilizing after approximately epoch 150. Evaluation on the test set yielded strong overall performance metrics, with mAP@50: 95.3%, precision: 81.3%, and recall: 94%.



(a) (b)

Figure 3. Training and evaluation performance of the model: (a) training and validation loss curves plotted against epochs and (b) performance metrics plotted against epochs

3.3. Class-wise model performance

Table 2 shows the confusion matrix resulted from the test process using Roboflow, utilized to estimate the mAP@50, precision, and recall at class-wise breakdown. The calculated estimation revealed variability in detection performance across the four parasite classes, whereas for *Fasciola* sp., mAP = 97%, precision = 92.3%, and recall = 80%. *Moniezia* sp. recorded mAP = 99%, precision = 100%, and recall = 90.2%. The *Paramphistomum* sp. recorded mAP = 100%, precision = 100%, and recall = 100%, while *Strongyle* sp. recorded the lowest performance at mAP = 90%, precision = 90%, and recall = 75%.

Table 2. The confusion matrix resulted from the test process, using Roboflow, of images to detect cattle parasitic eggs

Parasitic egg classes		Prediction					Total
		Fasciola	*Moniezia*	*Paramphistomum*	*Strongyle*	False negative	
Ground trutl	*Fasciola*	12	0	0	0	3	15
	Moniezia	0	55	0	0	6	61
	Paramphistomum	0	0	6	0	0	6
	Strongyle	1	0	0	9	2	12
	False positive	0	0	0	1	0	1
	Total	13	55	6	10	11	95

Qualitative visual assessment identified false negatives in images where parasitic eggs were not detected by the model. False positives were also observed, particularly when a single egg was misclassified between *Fasciola* sp. and *Strongyle* sp., likely due to their morphological similarity in shape, size, and coloration (Figure 4). Confusion matrix heatmap visualization was applied to selected test images to illustrate model attention. The heatmaps confirmed that YOLOv11 focused primarily on egg boundaries and internal texture rather than background debris, supporting clinical interpretability (Figure 5). In addition to precision, recall, and mAP@50, PR curves and receiver operating characteristic (ROC) curves were generated for each class. Confidence intervals (95%) were computed across cross-validation folds (Figure 6).

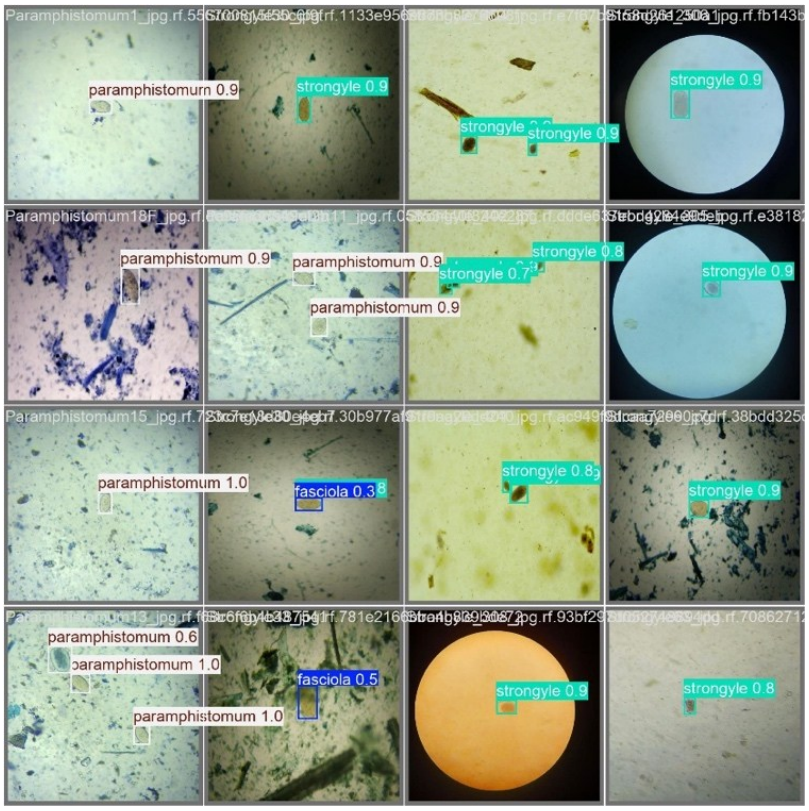


Figure 4. False negative of *Strongyle* sp. and positive detections of *Strongyle* sp. and *Fasciola* sp., where one egg was detected as *Fasciola* sp. and *Strongyle* sp. eggs

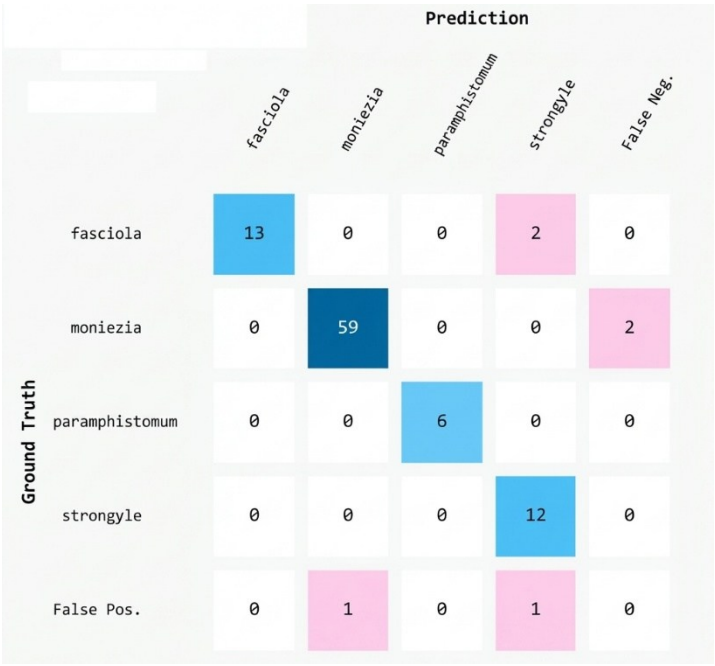


Figure 5. Confusion matrix heatmap for test images result detections

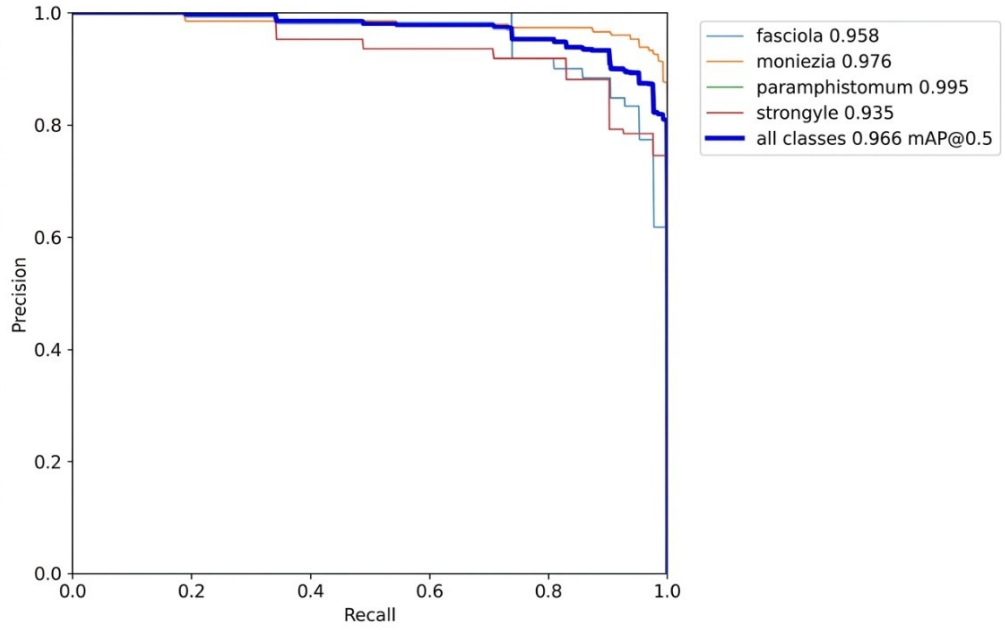


Figure 6. PR curves of model performance

Figure 6 presents the PR curves for the four parasite classes and the overall model performance at IoU = 0.5. The overall mAP@0.5 is 0.966, indicating excellent detection performance across all classes. Among the individual classes, *Paramphistomum* sp. achieved the highest AP (AP = 0.995), demonstrating near-perfect detection performance. The curve remains close to the top-right corner, indicating consistently high precision across recall levels. *Moniezia* sp. also showed strong performance (AP = 0.976), with minimal precision degradation as recall increases. *Fasciola* sp. achieved an AP of 0.958, indicating robust detection capability, although a slight precision decline is observed at very high recall levels. *Strongyle* sp. recorded the lowest AP among the four classes (AP = 0.935). The curve shows a more noticeable drop in precision as

recall approaches 1.0, suggesting greater classification difficulty. This is likely due to morphological similarities between *Strongyle* sp. and *Fasciola* sp., as previously discussed.

Analysis of the confusion matrix and PR curves highlights the strengths and operational limitations of the proposed diagnostic framework. The confusion matrix reveals that while distinct parasite structures (such as *Paramphistomum* sp. and *Moniezia* sp.) achieve high classification accuracy, morphological overlap between *Strongyle* sp. and *Fasciola* sp. remains a primary cause of misclassification. The PR curves for each class demonstrate variations in detection stability. *Paramphistomum* sp. and *Moniezia* sp. consistently maintains high precision across all recall levels, whereas *Strongyle* sp. exhibits a decline in precision at higher recall thresholds. Understanding these class-specific trade-off characteristics is crucial for adjusting decision thresholds in clinical practice to balance high diagnostic sensitivity against the risk of false positives.

3.4. Model architecture and comparative analysis

A comparative experiment was conducted to evaluate the impact of data augmentation on model performance. Two training configurations were assessed: i) training without data augmentation and ii) training with data augmentation, as previously described. The results are presented in Table 3. The findings indicate that applying augmentation slightly improved mAP@50 and precision. Specifically, mAP@50 increased from 89.3 to 91.3%, while precision improved from 92.4 to 95.6%. However, recall decreased from 92.1 to 86.3%, suggesting that augmentation enhanced detection confidence but slightly reduced sensitivity.

Table 3. Performance comparison on YOLOv11 between with and without data augmentation

Metric	Without augmentation (%)	With augmentation (%)
mAP@50	89.3	91.3
Precision	92.4	95.6
Recall	92.1	86.3

A comparative evaluation was also conducted on the YOLOv11, YOLOv8, and YOLOv5 algorithms using average confusion matrix results from 5-fold cross-validation to assess per-class detection accuracy. The cross-validation employed a stratified 5-fold split, maintaining proportional class representation across training and testing folds to prevent bias toward dominant classes. The results indicate that YOLOv11 achieved slightly better classification performance than YOLOv8 and YOLOv5 across various parasite categories (Table 4).

Table 4. Performance comparison between YOLOv11, YOLOv8, and YOLOv5

Metric	YOLOv11	YOLOv8	YOLOv5
Precision(B)	0.946852	0.944118	0.944523
Recall(B)	0.958143	0.955301	0.950925
mAP50(B)	0.979870	0.981359	0.981241
mAP50-95(B)	0.846814	0.846488	0.849996

3.5. Discussion

An AI-based tool has been developed to detect parasite eggs in livestock. Overall model performance confirms that the YOLOv11-based detection system achieves high diagnostic precision and recall, demonstrating its ability to minimize both false-positive and false-negative results. Convergence patterns indicate that the model successfully learned the distinguishing features of the four target parasite egg classes, despite the relatively small dataset size. The stability of validation metrics during the final epoch reinforces the model's generalization capability regarding new image data. A high mAP@50 value underscores the model's robust localization and classification capabilities for the microscopic detection of parasite eggs.

This model achieved a high level of sensitivity, particularly for *Moniezia* sp. and *Paramphistomum* sp., confirming its effectiveness against these parasite groups. However, the detection of *Strongyle* was relatively weaker, yielding low precision and recall values. This suboptimal performance is likely attributable to factors such as the limited number of *Strongyle* images in the test dataset, which reduced the model's exposure to representative morphological variations during the training phase. Furthermore, *Strongyle* eggs share visual characteristics with *Fasciola* eggs, specifically regarding shape and color distribution, when observed under a

light microscope. This resemblance increases the likelihood of false positives and false negatives, an issue also noted in previous CNN-based parasitology studies.

Confidence scores, representing the model's certainty in each detection, varied across classes. Predictions for *Moniezia* sp. and *Paramphistomum* sp. generally exceeded 90% confidence, aligning with their high precision and recall values. The robustness observed in the study can be attributed to multiple factors including the inclusion of diverse augmentation techniques (flips, rotations, exposure adjustments), which improved the model's ability to generalize to unseen variations. The apparent robustness may also be attributable to the use of transfer learning from COCO-pretrained data, which provided a strong initial feature extraction capability. In contrast, *Strongyle* predictions showed greater variance, with an average confidence of approximately 62%. This lower confidence score reflected the model's difficulty in differentiating *Strongyle* eggs from visually similar structures, highlighting an area for potential enhancement through targeted data augmentation or class-specific model fine-tuning.

Compared to conventional microscopy, the YOLOv11-based system demonstrates clear advantages in both accuracy and efficiency. Traditional microscopic examinations relying on human experts typically achieve an accuracy rate of 70–80% and require three to five minutes per sample. In contrast, this automated model maintains superior reproducibility and processes each image in less than 0.5 seconds. This represents a tenfold increase in diagnostic capacity, enabling large-scale screening with minimal turnaround time. Such efficiency gains are particularly beneficial for regions facing shortages of experts and limited laboratory capacity. Furthermore, the system's compatibility with smartphone-based microscopy aligns with previous research highlighting the importance of mobile-based diagnostics in resource-limited settings. By eliminating reliance on expensive laboratory equipment, this proposed method offers a scalable solution for rural areas and small-scale agricultural sectors, where timely parasite detection and control are often hindered by infrastructure limitations. The observed performance accorded with prior studies utilizing deep learning methods and automated platforms for parasitic helminth egg recognition [25]. Nagamori *et al.* [16] reported 85–90% AP in detecting canine and feline fecal parasites using a CNN-based system, while Kumar *et al.* [7] achieved mAP of 92.3% for detection of human intestinal parasites using YOLOv5.

The AP and mAP in the present study was slightly higher for three classes excluding *Strongyle* sp. than those reported previously despite the relatively small dataset and the class imbalance observed. Further, the strong results for *Moniezia* sp. and *Paramphistomum* sp. demonstrate that YOLOv11 can detect accurately multiple morphologically distinct parasite eggs within the same diagnostic context. The existing commercial AI-based veterinary diagnostic platforms reported recall of 88% of *Toxocara* sp., *Taenia* sp., and *Ancylostoma* sp. eggs. The present YOLOv11 system achieved higher recall for two of the four target species but lower overall precision for *Fasciola* sp. and *Strongyle* sp. This study reinforces prior observations that the YOLO architecture, when paired with transfer learning, can achieve high detection accuracy even in domain-specific, limited-data scenarios.

The *Strongyle* sp. performance issue suggests that future research should focus on collecting a larger, more diverse set of *Strongyle* sp. images, including various imaging conditions and magnifications. Furthermore, applying segmentation-based methods or incorporating attention mechanisms could help the model focus on subtle morphological differences, thereby improving discriminative capacity. Expanding the dataset, incorporating more diverse imaging conditions, and exploring segmentation-based architectures or attention mechanisms may further enhance performance.

Despite the promising results, several limitations warrant consideration. Although augmentation increased the total image count, the original dataset was relatively small and only four parasite species were included in the study. Further, all samples were collected in a single geographic region, potentially limiting the model's ability to generalize to other parasites with subtle morphological variations. The limitation may also arise for detecting the same parasite species from different regions which may vary in size and morphology. Increasing both the number and diversity of images, particularly for underrepresented classes could help to improve the performance of AI-powered detection of cattle parasitic eggs. Testing the model on datasets from different geographic regions would be needed to assess generalizability of the system. Future development should also include mobile application development, deploying the trained model as a smartphone application for real-time field diagnostics and integrating automated reporting and data storage for epidemiological tracking [21], [25], [26].

3.6. Implications for veterinary practice and livestock management

The implementation of such AI-based diagnostic systems can fundamentally transform parasite control strategies within livestock production systems. Faster and more accurate diagnosis enables early intervention, thereby reducing the prevalence and severity of infections, which in turn enhances animal welfare and productivity. This aligns with global efforts to strengthen food security through improved animal health monitoring and disease control. Furthermore, these systems can play a role in managing resistance. For

instance, the ability to monitor parasite loads more frequently can help detect the emergence of resistance to anthelmintic drugs, such as triclabendazole resistance in *Fasciola hepatica*, thereby allowing for timely adjustments to treatment protocols.

4. CONCLUSION

This study demonstrates that YOLOv11, integrated with Roboflow, provides a robust and efficient framework for automated detection of internal parasitic eggs in cattle. Cross-validation, comparative analysis, and interpretability assessment confirm model reliability and clinical relevance. The YOLOv11 detection system demonstrated high performance in identifying parasitic eggs from smartphone-captured microscopic images, with strong confidence score, time efficiency gains over traditional methods, and high repeatability. Future work should focus on increasing dataset diversity, focus on expanding geographically diverse datasets, integrating attention-based architectures, and deploying the system as a mobile veterinary diagnostic application.

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This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

INFORMED CONSENT

This study does not involve individual personal data or identifiable human subjects. Therefore, informed consent was not required.

ETHICAL APPROVAL

This study involved the collection of adult internal parasites from liver, gall bladder, intestine and faecal samples of cattle following regular slaughters conducted in a local abattoir in Malang, East Java, Indonesia. Permission was obtained from the abattoir management preceding the parasitic samplings in the abattoir. Faecal sampling was also conducted from a parasitic-egg-free bull from a farm in Malang. The parasitic-free faecal samples would be mixed with adult parasites to produce a condition mimicking natural condition of faecal samples positive to parasitic eggs. Before the faecal sampling of parasitic-free faeces, the animal was known to be treated with Albendazole at 20 mg/kg body weight and observed using

sedimentation and floatation methods for two months in four-time intervals, to ensure that it was free from any internal parasite. During faecal sampling in the farm, only naturally excreted faecal samples were collected, and no research procedure required cattle handling. Oral informed consents for faecal sample acquisition were obtained from the cattle owner.

DATA AVAILABILITY

The data that support the findings of this study were obtained by authors and will be publicly available in Roboflow repository at https://app.roboflow.com/egg-worm-detection following a 3 month from the date of publication. Requests for access may be directed to the corresponding author, subject to approval from the original authors.

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